

**Method of producing double low restorer lines of *Brassica napus*
having a good agronomic value**

The invention relates to a method of producing a double low restorer lines of

5 *Brassica napus* for Ogura cytoplasmic male sterility (cms) presenting a radish introgression carrying the Rfo restorer genes deleted of the radish Pgi-2 allele and recombined with the Pgi-2 gene from *Brassica oleracea*, and having a good agronomic value characterized by female fertility, a good transmission rate of Rfo and a high vegetative vigour. The invention relates also to a method of forming

10 *Brassica napus* hybrid seed and progeny thereof and to the use of markers for selection.

Breeding restorer lines for the Ogu-INRA Cytoplasmic Male Sterility (cms) system in rapeseed (*Brassica napus* L.) has been a major objective during the past few years. Extensive backcross and pedigree breeding were necessary to improve their

15 female fertility and to get double low restorer lines. The so-called «double low» varieties are those low in erucic acid in the oil and low in glucosinolates in the solid meal remaining after oil extraction. However some difficulties can still be encountered in breeding these lines (introgression rearrangements, possible linkage with negative traits) due to the large size of the radish introgression.

20 The inventors thus assigned themselves the objective of providing a new improved double low restorer line with a good agronomic value.

This objective is obtained by a new method of producing a recombined double low restorer line for the Ogu-INRA cms in rapeseed.

A first object of the present invention relates to a method of producing double low restorer lines of *Brassica napus* for Ogura cytoplasmic male sterility (cms) presenting radish introgression carrying the Rfo restorer gene deleted of the radish Pgi-2 allele and recombined with the Pgi-2 gene from *Brassica oleracea*, and having a good agronomic value characterised by female fertility, a good transmission rate of Rfo and a high vegetative vigour, said method including the step of:

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30 a) crossing double low cms lines of spring *Brassica napus* comprising a deleted radish insertion with the double low line of spring Drakkar for forming heterozygous restored plants of *Brassica napus*,

- b) irradiating before meiosis the heterozygous restored plants obtained in step a) with gamma ray irradiation,
- c) crossing pollen from flowers obtained in step b) with the cms double low spring Wesroona line,

5 d) testing the progeny for vigour, female fertility and transmission rate of the cms gene,

 e) selecting progeny lines.

In the present invention, the term "lines(s)" means a plant which is essentially homozygote and which is reproducible by auto-pollination.

10 A method according to claim 1, wherein the irradiation dose in step b) is 65 Gray during 6 mn.

According to one advantageous form of embodiment of the method according to the present invention, the double low cms line of spring *Brassica napus* of step a) is R211.

15 R211 is an INRA spring restorer line.

Drakkar is a French spring registered variety.

Wesroona is an Australian spring registered variety.

According to one advantageous form of embodiment of the method according to the present invention, the testing is performed with the combination of five markers

20 selected from PGIol, PGIUNT, PGIntl, BolJon and CP418.

Another object of the present invention relates to double low restorer lines of *Brassica napus* for Ogura cms presenting a Rfo insertion deleted of the radish Pgi-2 allele and recombined with the Pgi-2 gene from *Brassica oleracea*, and having a good agronomic value characterised by female fertility, a good transmission rate of

25 Rfo and a high vegetative vigour.

According to one advantageous form of embodiment, the double low restorer lines present a unique combination of five markers selected from PGIol, PGIUNT, PGIntl, BolJon and CP418.

Another object of the present invention relates to a method of forming *Brassica* 30 *napus* hybrid plants and progeny thereof obtained through the steps of:

a) providing a restorer line produced according to claim 1 and bred to be homozygous,

b) using said restorer line in a hybrid production field as the pollinator,

c) using cms sterile plants in a hybrid production field as the hybrid seed producing plant, and

d) harvesting the hybrid seed from the male sterile plant.

5 Another object of the present invention relates to seeds of Brassica plant obtained from the methods according to the present invention.

Still another object of the invention relates to seeds of Brassica napus deposited in NCIMB Limited, 23 St Machar Drive, Aberdeen, Scotland, AB24 3RY, UK, on July 4, 2003, under the reference number NCIMB41183.

10 Another object of the present invention relates to the use of at least four markers PG1ol, PG1int, BolJon and CP418, or any portion of them comprising at least one polymorphic site, for characterising recombined restorer lines of Brassica napus for Ogura cms presenting a Rfo insertion deleted of the radish Pgi-2 allele and recombined with the Pgi-2 gene from Brassica oleracea, and having a good

15 agronomic value characterised by female fertility, a good transmission rate of Rfo and a high vegetative vigour.

In a preferred embodiment, the combination is of five markers PG1ol, PG1UNT, PG1int, BolJon and CP418.

In the present invention, the expression " any portion of them comprising at least

20 one polymorphic site" means any part of the sequence showing at least a difference between the B.oleracea type sequence and B.rapa type sequence.

Such markers are represented in the following figures and sequence listing for the R2000 line.

According to one advantageous form of embodiment, the present invention relates

25 to:

- The marker PG1ol which is amplified using the primers: PG1ol U and PG1ol L
(PG1ol U: 5'TCATTTGATTGTTGCGCCTG3';
PG1ol L: 5'TGTACATCAGACCCGGTAGAAAA3')
- The marker PG1int which is amplified using the primers: PG1int U and PG1int L
(PG1int U: 5'CAGCACTAATCTTGCAGGTATG3';
PG1int L: 5'CAATAACCCTAAAAGCACCTG3')
- The marker PG1UNT which is amplified using the primers: PG1ol U and PG1int L:

(PGIol U: 5'TCATTTGATTGTTGCGCCTG3';
 PGIint L: 5'CAATAACCCTAAAAGCACCTG3')

- The marker BolJon which is amplified using the primers: BolJon U and BolJon L:
 (BolJon U: 5'GATCCGATTCTCTCCTGTTG3';
 5 BolJon L: 5'GCCTACTCCTCAAATCACTCT3')
- The marker CP418 which is amplified using the primers: SG129 U and pCP418 L:
 (SG129 U: cf Giancola et al, 2003 *Theor Appl. Genet. (in press)*
 pCP418 L : 5'AATTTCTCCATCACAAAGGACC3')

Another object of the present invention relates to the PGIol, PGIUNT, PGIint, BolJon
 10 and CP418 markers whose sequences follow:

PGIol R2000 marker:

TCATTTGATT	GTTGCGCCTG	TCGCCTTGTT	GTGTTATGAT	GAATGAACAG	CAGTCATTAA	60
ACATGTGGTT	AACTAACAG	GGCTCCGGCT	GTTGAAAAC	ACATGGTTGC	TGTCAGCACT	120
AATCTTGCAG	TATGAATTG	TGATTAATT	TGTTTGTGTTG	TGACTCTTTC	TTCATTGTTG	180
15 GTTTTCGTAC	AATAAACCGA	ATGTATAATC	TTTACAAAC	TGAATTTC	ACCGGGTCTG	240
'GATGTACA						248

PGIUNT R2000 marker:

TCATTTGATT	GTTGCGCCTG	TCGCCTTGTT	GTGTTATGAT	GAATGAACAG	CAGTCATTAA	60
20 ACATGTGGTT	AACTAACAG	GGCTCCGGCT	GTTGAAAAC	ACATGGTTGC	TGTCAGCACT	120
AATCTTGCAG	TATGAATTG	TGATTAATT	TGTTTGTGTTG	TGACTCTTTC	TTCATTGTTG	180
25 GTTTTCGTAC	AATAAACCGA	ATGTATAATC	TTTACAAAC	TGAATTTC	ACCGGGTCTG	240
ATGTACAATG	CTAGTCTCCA	TGTTCTGGG	GATCATGATT	TATTTCTAC	ATGTATTTCAG	300
ACAGTACAGA	AGAAAAGTGT	CAAAACTCTG	GATGTTTAA	TTTACAGTTA	GTGGAGAAAGT	360
25 TCGGCATTTGA	TCCGAACAAAT	GCATTTGCAT	TTTGGGACTG	GGTGGTGGGA	AGGTACAGTG	420
GTAAGTGCTT	GTTTATTG	TTGTATAAAAT	TTCTCGTCCA	TTTCCGCTTG	CTTAGTGTAT	480
AACTGAAATT	CTTTGCACT	TTGCAGTGT	GTTGGAGTCT	TACCATGTC	TCTACAGTAT	540
GGCTTCTCTG	TGGTGAGAA	GTACGGTACC	TTCTACTTTA	TCAGCCATCT	CATAAAATGT	600
CTTAGGCATA	TTCTTTCTAT	TTTATTTCCC	TCTTAATGAT	TTCTCTTTT	TTTATTGCA	660
30 TTCCCCTTT	ATTTCAAA	GTGTTACTG	TCTCTAAATC	AAGAAGAAAC	CTTCTTAGTA	720
GATCCAGCTG	ATATTCAAGCC	TTTTTAAAT	TGGACTGCAG	GTTTTAAAG	GGGAGCTTC	780
AGCATTGATA	AGCATTCCA	GTCCACACCG	TTTGAGAAGA	ATATACCCGT	GAGTTGCATT	840
AGTTGTGTGA	TTATACAGTT	TTCTTGCTT	TTTGCTATGT	CCATCAACAC	TAGAGATTG	900
TGAAGTTATT	AGTGTAGTC	ACGCATAGGG	AGAGGTGATT	GGTGACTTT	GGACGATTTC	960
35 AGGTGCTTTA	GGGTTATTG					979

PGIint R2000 marker:

CAGCACTAAT	CTTGGCGGTAT	GAATTTGTGA	TTAAATTTGT	TTGTTTGTGA	CTCTTTCTTC	60
40 ATTGTTCGTT	TTCGTACAAT	AAACCGAATG	TATAATCTT	TACAAACTGA	ATTTTCTACC	120
GGGTCTGATG	TACAATGCTA	GTCTCCATGT	TCTTGGGGAT	CATGATTAT	TTTCTACATG	180
TATTTCAGACA	GTACAGAAGA	AAGTGTCAA	AACTCTGGAT	GTTTTAATT	ACAGTTAGTG	240
GAGAAGTTCG	GCATTGATCC	GAACAATGCA	TTTCATTTT	GGGACTGGGT	TGGTGGAAAGG	300
TACAGTGGTA	AGTGCTTGT	TATTTGGTTG	TATAAATTTC	TCGTCATTT	CCGCTTGCTT	360
AGTGTATAAC	TGAAATTCTT	TTGCAGTTG	CAGTGTGT	GGAGTCTTAC	CATTGTCTCT	420
45 ACAGTATGGC	TTCTCTGTGG	TTGAGAAGTA	CGGTACCTTC	TACTTATCA	GCCATCTCAT	480
AAAATGTCTT	AGGCATATTTC	TTCTATTTT	ATTTCCCTCT	TAATGATTTC	TTCTTTTTT	540
TATTGCATTC	CCGTTTTATT	TTCAAAAGTT	GTACTGTCT	CTAAATCAAG	AAGAACCTT	600

5 CTTAGTAGAT CCAGCTGATA TTCAGCCTT TTTAAATTGG ACTGCAGGTT TTTAAAGGGG 660
 AGCTTCAAGC ATTGATAAGC ATTTCCAGTC CACACCGTT GAGAAGAATA TACCCGTGAG 720
 TTGCATTAGT TGTGTGATTA TACAGTTTC TTGTCCTTTT GCTATGTCCA TCAACACTAG 780
 AGATTCTGTA AGTTATTAGT GTAGTCAACG CATAGGGAGA GGTGATTGGT GACTTTGGA 840
 CGATTCAGG TGCTTAGGG TTATTG 866

BolJon R2000 marker:

10 GATCCGATTG TTCTCCTGTT GAGATCAGCT CCAAACATCA AACAACTTGT ACACAAATAT 60
 CTTTACTTGC TAAATGGAAC ATGACAAGAG ATAGAAAATC TTGCTCATAG TATTGTACAA 120
 GGGATAACAG TGTAGAAAAC AAACCGCTG TAAGATTTT TCCCTGATCC TCTCACTTAA 180
 CCAGTAGGGCG TTTTCACAT TGAAGCGCAT ATCTACTTTG GTATTCACTG AATAAAAAAA 240
 GAAAGCTGGT AACATGTGAA GGATATACAA GCATTGATAC ACCAAGTAGT CACAAACTAC 300
 ATATATAAAGG TCAGACCTT GTTCACATTC TGGCCTCCAG GACCACCGCT TCTAGCAAAG 360
 TTAAGCGTAA CATGGTCTGC ACGTATACAA ATGAAAATGT TTCTATCAAATCCTATAAA 420
 15 ATAGAGCTCT ATAACATTGT CGATACATAG TTTCACTAAC TCTGCAAGTA CAAACACAT 480
 ATACAAACAA AACTATGCGA ACAGATCAA ACTACTACAG AACACAGTTC TATGACACTG 540
 TCGATAGTAA CATCCCTGTC AAGTACAAA GAGATAGCAA ATGAAACAT GTAAACAAAT 600
 CAAAATTCTA AATTCTCCA TCACAAGGAC CTACAGAATA GAGTTATCAT AACATTTCT 660
 GTAAATATTG CCATCTAAAT GACTAGAGAA CAGAGTTCT ATAACATTAT CTGTAATGT 720
 20 TCCAACAAAA CCACATACATA GCAGAGTTCT TATAACATTG TCTGTAATG TCCAATCAA 780
 ACCACTACAG AACAAAGCTC CTATAACATT GTTATACAA AGTTCACTA AATCTACAA 840
 CTTCCCCGT AAATGAGCTT AATATCACCC AAAGATGTTT CAATCAGATA AAGAGTACGA 900
 CATCGTTTG AGATTAGAAC AAACGTGAAAC TTACGTAGAG TGATTGAGG AGTAGGC 957

CP418L R2000 marker:

25 AATTCTCCA TCACAAGGAC CTACAGAATA GAGTTATCAT AACATTTCT GTAAATATT 60
 CCATCTAAAT GACTAGAGAA CAGAGTTCTT ATAACATTAT CTGTAATGT TCCAACAAAA 120
 CCACTACATA GCAGAGTTCT TATAACATTG TCTGTAATG TCCAATCAA ACCACTACAG 180
 AACAAAGCTC CTATAACATT GTTATACAA AGTTCACTA AATCTACAA CTTTCCCCGT 240
 30 AAATGAGCTT AAATCACCC AAAGATGTTT CAATCAGATA AAGAGTAACG ACATCGTTT 300
 GAGATTAGAA CAAACTGAAA CTTACGTAGA GTGATTTGAG GAGTAGGCTC GTGCCAGCA 360
 GAGCTAGCTC TCTCCCTCCGC CTATGAAGC ATCTGTTGCA CCTGAGACAA CCGTGACGAA 420
 ACTTCCGAT CACGCCACC AGAATTGAC GCGCGCATC GGAAGGATCC GAATCGGGAA 480
 35 CTGAGTGAAC CCGAGCGATC CCGGGAGTGC GACGGAGCGA TGGGAAAAGA GAGTGGCACG 540
 ATTCGACGA AGAGTGGAAAG AGGAGAGGGT GGTGGATAAA CTCGCGTATG ATCAAGTTCG 600
 TCATCGTCTT GATTGCCGCC ATTTTTTTG TCAGGGCGCT CTGTGGCTTA GAAGTTCCG 660
 ATGTCAATGA AC 672

In the annexed drawing that follows, the following abbreviations are used :

40	Dra	Drakkar
	Rel-15-1, E38,R15	R2000
	Hete, Hel, R211.Drakkar	heterozygous R211*Drakkar,
	Darm	Darmor
	Bol:	Brassica oleracea
45	Bra, B.rap:	Brassica rapa
	GCRA18-A19, Wes, Aust:	Wesroona
	Sam, SamlPGIolSunt5	Samourai
	RRH1, ba2c	RRH1
	rav, N.WR	Hybrid Brassica napus*wild Radish

- Figure 1 illustrates Gamma ray Irradiation and F2 production.
- Figure 2 illustrates seed set on 'R211' and 'R2000'.
- Figure 3 illustrates the number of seeds per pod of different lines.
- Figure 4 illustrates PGiol primer localisation on the segment of PGI sequence from

5 Data Base. In that figure:

PGiol: - primer PGiol U (named in SGAP: BnPGICh 1 U)
 - primer PGiol L (named in SGAP: Bn PGICh 1 L)

PGlint: - primer PGlint U
 - primer PGlint L (is out side the sequence).

10 - Figure 5 illustrates electrophoresis gel of PGI-2 gene (PGiol), PCR marker and SG34, a PCR marker close to Rfo.
- Figure 6 illustrates Pgi-2 segment of DNA amplified by PCR with PGiol primers.
- Figure 7 illustrates digestion of the PCR product PGiol by Mse1.

In that figure:

15 Sam and Darm has a 75bp band.

Drak, R211.Dk and R2000 showed a 70pb one (Acrylamide 15%).

8 was similar to Samourai (75bp) ; mix with Drakkar (70pb) it allowed the visualisation of the two bands.

- Figure 8 illustrates electrophoresis agarose gel of PGIUNT marker.

20 In that figure:

PGIUNT band (about 980bp) is present in Boleracea, B.rapa cv Asko, maintainer and restored lines except in 'R211'.

There is no amplification in radish and Arabidopsis.

In various Brassica genotypes only one band was amplified. Size band are similar

25 but sequences are different.

- Figure 9 illustrates electrophoresis gel of PGlint PCR marker.

In that figure PGlint of radish line 7 is of about 950bp. This band is the same as in the restored RRH1 and R113. It is not found in R211. It is not either in R2000. However the PGlint band is of a similar size of about 870bp in the various Brassica

30 species, but sequences are different.

- Figure 10 illustrates electrophoresis agarose gel of Bo1Jon PCR marker.

- Figure 11 illustrates electrophoresis agarose gel of CP418 marker.

In that figure, the CP418 band (of about 670bp) is specific to the B.oleracea genome. It is present in B.ol, B.napus (Samourai, Drakkar, Pactol and the herterozygous R2111*Dk). It is absent from the restored rapeseed (RRH, R113 and R211). It is present in the homozygous R2000.

- 5 - Figure 12 illustrates summary markers table.
 - Figure 13 (13(a),13(b)) illustrates PGIol marker sequence alignment between Arabidopsis, Radish, B.rapa, B.oleracea and R2000.
 - Figure 14 (14(a), 14(b), 14(c), 14(d)) illustrates the PGInt-UNT marker sequence alignment between Arabidopsis, Radish, B.rapa, B.oleracea and R2000.
- 10 - Figure 15 (15(a), 15(b), 15(c)) illustrates the CP418L marker sequence alignment between Arabidopsis, Radish, B.rapa, B.oleracea and R2000.
 - Figure 16 (16 et 16bis) illustrates Arabidopsis, Radish and B.rapa BolJon markers. There are aligned with DB sequences of Arabidopsis (AC007190end-AC011000beginning), the B.oleracea EMBH959102 end and EMBH448336
- 15 15 beginning and representative consensus sequences of the SG129markers band 1 and 2 in B.napus (in Drakkar and Samourai respectively).
From the point 836bp, AC07190-AC11000 and GCPATpBOJ sequences are no longer closely homologous to the Brassica sequences.
The radish and B.rapa (GCPconsen RsRf BOJ and BR) sequences are still closely
- 20 20 homologous to the B.napus one, from 858bp point to the 900bp and 981 points respectively.
In radish, only partial homology is found on the Brassica sequence further down.
In B.rapa species cv Asko, the left of its BolJon sequence can be aligned again, after a 78bp deletion, with those of B.oleracea and B.rapa in B. napus from the 1057bp
- 25 25 point to the BolJon L primer.
 - Figure 17 (17 et 17bis) illustrates the localisation of Pgi-2 primers on the Arabidopsis th MJB21.12 sequence.
 - Figure 18 illustrates the BolJon primers localisation on the mipsAt162850 gene and overlapping area of AC007190 and AC011000 Arabidopsis th clones.
- 30 30 Alignment with the Arabidopsis BolJon PCR product (740bp) is presented.

It should be understood, however, that the examples are given solely by way of illustration of the object of the invention, of which they in no way constitute a limitation.

- 5 **Example I: method of producing a double low restorer line of *Brassica napus* for Ogura cytoplasmic male sterility (cms) presenting a radish introgression, carrying the Rfo restorer gene deleted of the radish Pgi-2 allele and recombined with the Pgi-2 gene from *Brassica oleracea*, and having a good agronomic value characterised by female fertility, a good transmission rate of**
- 10 **Rfo and a high vegetative vigour.**

Materials and methods :

Genotypes: The 'R211' line with a deleted radish insertion was crossed to the spring low GLS rapeseed 'Drakkar' to produce a F1 progeny ('R211*Dk'). The spring low GLS cms line 'Wesroona' (australian origin) was used for following crosses. Were 15 used as control in molecular analyses: Winter restored lines derived from 'Samourai' carrying the complete ('RRH1') or incomplete ('R113') introgression as well as European radish line7, Asiatic restored radish D81, hybrid *Brasica napus** wild radish, *Brassica oleracea*, and *B.rapa* cv Asko, *Arabidopsis thaliana*.

Gamma ray irradiation: Whole flowering plants were treated with gamma rays from 20 a Co60 source in a controlled area. Sublethal dose fo 65 Gray was applied before meioses.

Testcrosses and F2 production: Irradiated plants were transferred in an insectproof greenhouse after removing flower buds larger than 2 mm. The irradiated F1 progeny was used to handpollinate the cms 'Wesroona' line. The restored derived F1' plants 25 were allowed to produce F2 families harvested individually and precisely sown in a field assay along with non irradiated controls (Fig 1).

Phenotypic selection: Three visual criteria were scored (on a 1 to 5 scale) over 2 years in field assays, on 1200 F2 offsprings plus 44 controls (82 330 quoted plants):
1-Vegetative vigour,
30 2- Normality of the ratio of fertile /sterile plants in the F2 segregation, and
3- Female fertility (pod development and seed set).

Advanced selfed generations of the selected families were obtained either in field or greenhouse and produced homozygous lines (F4) for further analysis.

Isozyme analysis was performed as in (Delourme R. and Eber F. 1992. *Theor Appl Genet* 85: 222-228), marker development from (Fourmann M et al 2002.

5 *Theor Appl. Genet.* 105:1196-1206.): PCR products are validated by sequencing. Alignments were made using Blast Ncbi and Uk Crop Net Brassica DB and the Multalin software INRA Toulouse.

Method :

We choose one low GLS spring homozygous restorer line, 'R211', already 10 exhibiting deletions in the introgression (Delourme R. and Eber F. 1992. *Theor Appl Genet* 85: 222-228. Delourme R et al 1998. *Theor Appl Genet* 97: 129-134. Delourme R. et al 1999. *10th Int. Rapeseed Congress, Canberra.*). Several molecular markers are missing on either side of Rfo, such as spATCHIA (Fourmann M et al 2002. *Theor Appl. Genet.* 105:1196-1206), spSG91 (Giancola S et al 2003 *Theor Appl. Genet. (in press)*)). 'R211' lost the isozyme expression of the Pgi-2 allele of 15 the radish gene but also the one of Pgi-2 allele of B.oleracea genome (1,2). Moreover, the homozygous 'R211' shows linked negative traits such as low vigour and very poor seed set. We hypothesised that these plant lack a rapeseed chromosomal segment. The fertile ratio in F2 progenies derived from this material 20 is lower than expected (64% instead of 75%). We initiated the program from this 'R211' line and tried to force recombination between the Rfo carrying introgression from this deleted line and the rapeseed homologous chromosome from a double low B. napus line.

Ionising irradiation is known to induce chromosomal rearrangements by double 25 strand breaks followed by aberrant rejoining of the ends. Gamma-ray irradiation was used on a heterozygous F1 derived from the 'R211' line to induce chromosome breaks, just before meiosis, aiming at a recombination of the deleted radish introgression in the rapeseed genome.

Results :

30 Very few families were at the best score for the three criteria out of 1200 F2 families tested.

Only one, 'R2000', proved to produce a normal ratio of fertile plants per selfed progeny with a stable recovery of good agronomic traits such as a good female fertility, with a normal seed set compared to 'R211' (Fig 2 and 3). This family was obtained from a 6 mn irradiation treatment at a dose flow of 65 Gray per hour.

5 Glucosinolate analysis confirmed its low content.

In figure 2 (Seed set on 'R211' and 'R2000') R2000 showed normal inflorescences, with a normal looking architecture.

In figure 3 (Number of seeds per pod), we observe:

- on the best 'R2000' F4 families in self pollination (Selfings) and in testcrosses
- 10 - on 'Pactol' cms line on rapeseed and 'R211' controls.

Example II: selection of markers in the Pgi-2 gene

PGI isoenzyme analysis: 'R2000' progeny expressed the rapeseed Pgi-2 allele from *B. oleracea* genome, originally lost in 'R211'.

15 Three PCR markers were defined to characterise the R2000 family compared to the known restorer rapeseed RRH1 and R113.

1) PGIdl marker was developed from the BrassicaDB sequences to be specific to the Brassica genome. There is no amplification in radish nor in *Arabidopsis th.*, but only in Brassica, with one 248 bp band.

20 2) PGInt marker amplified a longer part of the Pgi-2 gene, allowing clear distinction between the various tested species *Brassica*, *Raphanus* and *Arabidopsis*. The species *B.rapa* and *B.oleracea* were not distinguished by the band size on agarose gel, but by their PGInt band sequence.

3) PGInt marker, a combination of the PGI ol U and PGI int L primers.

25 This marker had the specificity of the PGIdl marker but amplifying a longer part as for PGInt one.

II.1 PGIdl marker

With the PGIdl primers, the 'R211' parental line showed no amplification, while the spring tested lines showed a 248bp band. Its DNA sequence is homologous to 30 the PGI-2 sequences from the Crop Net UK DB in Brassica species and from previous work in our group (named SGAP sequences) (Localisation of the primers SG PGI chou, Fig 4).

It was ortholog of the clone MJB21-12, on the chromosome V, (34543bp) in *Arabidopsis* (NCBI DB).

PGIol plus SG34 to set an Homozygosity test:

The combined use of two sets of primers in a mix PCR, PGIol marking the Pgi-2 gene absent in the homozygote restored plant and SG34 (from S. Giancola et al, Giancola S et al 2003 *Theor Appl. Genet. (in press)*), a very close marker to the Rfo gene, was set up to discriminate homozygous from heterozygous plant among the fertile plants segregating in F2 progenies derived from 'R211'. In place of using SG34, it is possible to use any other marker close to or in the Rfo gene.

Only one family R2000 showed no difference between homozygote and heterozygote offsprings:

The Pgi-2 gene is present in the R2000 homozygote, which is not the case for the parental homozygous R211.

In figure 5 (PGIol and SG34 PCR markers):

The homozygous 'R2000' family has recovered the PGIol band. DNA sequence of the band confirmed the homology with the known *Arabidopsis* and *Brassica* Pgi-2 sequence. Control genotypes (Drakkar, Pactol, and, Samourai, Darmor) had the same pattern on the gel. Sequence of this common band allowed to confirm their high homology as they were quasi similar except one base substitution.

The homozygous 'R2000' family has recovered the PGIol band of the *Brassica oleracea* type. It was distinct from the known restorer of the Samourai group.

This amplified part of the Pgi-2 is very conserved and hardly any differences were shown among the various genotypes. A longer part of Pgi-2 gene was investigated.

25 II.2 PGIUNT and PGIint markers

Electrophoresis Patterns of PCR products:

PGIUNT marker: A second reverse primer, PGIint L, was designed further down the Pgi-2 sequence, to amplify as well conserved and as variable regions of the gene. When used with the PGIol U primer, it amplifies a 980bp band only in *Brassica* genomes.

R211 didn't show any band, The homozygous 'R2000' showed the PGIUNT band as in the Drakkar parent.

In figure 8 (PGIUNT marker):

PGIUNT marker amplified a segment of PGIUNT. The upper primer PGIUNT allows the amplification in all tested species, allowing a clear distinction between *Arabidopsis*, Radish and *Brassica*. *B.rapa* and *B.oleracea* were not distinguished by the band size

5 on agarose gel, but by their PGIUNT sequence. All tested restored genotypes, but the 'R211' line, exhibited the European radish band and one *Brassica* band, homologous to the *B.rapa* one.

The homozygous 'R2000' didn't show the radish PGIUNT band, as in the deleted 'R211' parental line, but showed one *Brassica* band, homologous to the *B. oleracea*

10 one.

Electrophoresis of PGIUNT marker is represented in figure 9.

Sequence analysis:

Comparison of the PGI sequences from the data bases.

A PGI segment of about 490bp is known.

15 Sequences of a segment of about 490bp from different genotypes (*B. oleracea*, *B. rapa*, *B. napus*) have been studied in our laboratory group and some sequences were given to Brassica Crop Net DB: EMAF25875 to 25788 by M.Fouramnn (4) These sequences are very conserved.

Comparison of the *B. rapa* et *B.oleracea* species PGI sequences (figures 13 and 14):

20 Comparison between PGI sequences we have obtained from the tested genotypes of *B.oleracea* and *B.rapa* species, showed that they were distinct by 21 base substitutions. These substitutions allowed to distinguish PGIUNT sequences from the other tested genotypes of rapeseed, homologous to either *B.rapa* cv Asko (RRH1 and R113) or *B.oleracea* (Drakkar, R211*DK but also R2000).

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Example III: selection of marker in a region close to Rfo

Markers surrounding the Rfo gene in the radish insertion were determined in order to facilitate the Rfo gene cloning (Desloires S et al 2003 *EMBO reports* 4, 6:588-594). One of these, the SG129 PCR marker was located very close to Rfo

30 (Giancola S et al 2003 *Theor Appl. Genet. (in press)*): it co-amplified distinct bands in *B.oleracea* and *B.rapa* genomes of *B.napus*, but the radish band was very difficult to see on an agarose gel.

The target SG129 sequence was ortholog of a clone (AC011000, at the locus F16P17) in *Arabidopsis thaliana*. This clone overlapped an *Arabidopsis* adjacent contig clone (AC07190).

From the Brassica Crop Net DB, we found one *B.oleracea* clone, (EMBH448336, 5 764bp) blasting with the begining of the A011000, and a second *B.oleracea* clone (EMBH53971), distant from about 300bp on the *Arabidopsis* map, that blasted with the end of ACO7190.

We designed a new PCR marker, BolJon, between the two *B.oleracea* clones. We 10 verified that it allowed amplification of a specific PCR bands in the different genotypes compared here.

In figure 16 (electrophoresis gel of BolJon PCR products):

- In *Arabidopsis*, a BolJon 815bp band was amplified, homologue to the overlapping segment of the contigs.
- In Brassiceae diploid species, BolJon marker showed distinct bands: one of 15 950bp in *B.oleracea* and one of 870bp in *B.rapa*. It showed that the two *B.oleracea* clones (EMBH53971 and EMBH448336) are in sequence continuity in Brassica genome as it is for the ortholog sequences in *Arabidopsis*.
- In *B.napus*, these two bands are co-amplified in the maintainer lines, Samourai or Drakkar.
- 20 - In radish line7, one BolJon band was amplified of about 630 bp long. The band of the restored radish cmsRd81 was slightly smaller.
- In all the restored rapeseed lines, one of the BolJon bands was of the same size as the radish line7. BolJon is a marker of the radish introgression.
- The homozygous restored rapeseed lines, 'RRH1', 'R113' and also 'R211', 25 only showed the *B.rapa* band and the 630bp radish band bp suggesting the *B.oleracea* ortholog of the target gene is absent or has been modified when the radish segment of chromosome was inserted into the rapeseed *B.oleracea* constitutive genome.

'R2000' homozygote plants showed radish PCR BolJon, plus the two Brassica 30 BolJon bands, again having recovered the *B.oleracea* one, lost in 'R211' and other restorer lines.

We designed a primer, pCP418L, specific of the *B.oleracea* genome in the tested species. With the SG129U primer it amplified only one PCR band (670bp) in the *B.oleracea* species. (Fig 17)

There was no amplification in *B.rapa*, in radish, nor in *Arabidopsis*, but there was a 5 clear CP418 band in *B. napus* maintainer lines. Its sequence was strictly homologous to the EMBH448336 sequence. This marker was in a very conserved DNA sequence allowing no polymorphism between genotypes except by presence / absence.

In RRH1, R113 and in R211 there was no CP418 band, indicating as previously that 10 the *B.oleracea* ortholog of the target gene is absent or has been modified following the radish insertion.

‘R2000’ homozygote plants showed CP418 band, again having recovered the specific *B.oleracea* one.

In the present invention, a new recombined low GLS restorer line has been selected 15 with a good female fertility. The poor value of line ‘R211’ allowed selection in the field for a rare recombination event and characterisation the ‘R2000’ family.

The homozygous ‘R2000’ presents a unique combination of the PGIol, PGIUNT, PGIint and BolJon markers when compared with the rapeseed restorer analysed yet: PGIint marker showed that the homozygous restored rapeseed lines, RRH1 and 20 R113 presented the European radish band plus one *Brassica* band, homologous to *B.rapa* genome. ‘R2000’ shows no radish band, lost as in its parental deleted line R211, but showed one *Brassica* band homologous to *B.oleracea*. The ortholog PGIint sequence in its *B.rapa* genome is not amplified with this marker in R211 and Drakkar genetic background.

25 PGIol marker and PGIUNT marker sequences in restored lines RRH1 and R113 were homologous to the *B.rapa* cv Asko one. In ‘R2000’, PGIUNT sequence is homologous to *B.oleracea*. The ortholog PGIUnt sequence in its *B.rapa* genome is not amplified with this marker in R211 and Drakkar genetic background.

BolJon marker showed that the homozygous restored rapeseed lines, including 30 ‘R211’ presented the European radish band plus only the *B.rapa* one. ‘R2000’ shows the two bands of ‘R211’ plus the recovered *B.oleracea* BolJon band.

CP418 marker showed that ‘R2000’ recovered this conserved *B.oleracea* segment.

Our hypothesis is that a recombination event took place in the pollen mother cell which gave rise to 'R2000' plants. The deleted radish introgression was then integrated to the normal homologous chromosome segment, carrying the *B.oleracea* type *Pgi-2* gene and *BolJon* target sequence, characterised by these markers, 5 probably from the Drakkar '00' genome present in the irradiated heterozygous 'R211*DK'.

The pattern observed for *BolJon* suggests that the recombination event resulted in a particular duplicated region, one from radish and one *B.oleracea*, in the 'R2000' family.